Amendments to the claims begin on page 2.

Amendments to the specification begin on page 5.

Remarks begin on page 11.

Amendments to the claims:

1. (Withdrawn) A method for increasing the specific activity of a glycosyl hydrolase on a substrate, comprising replacing a hydrophobic surface binding amino acid of the hydrolase with a positively charged amino acid, to provide a mutant glycosyl hydrolase~~,~~.

2. (Withdrawn) The method of claim 1, wherein the hydrophobic surface binding amino acid includes tryptophan or tyrosine and the positively charged amino acid is arginine.

3. (Currently Amended) A method for increasing the specific activity of a mutated glycosyl hydrolase on a substrate relative to an unmutated form of the glycosyl hydrolase, comprising replacing an active site associated glycosyl-stabilizing amino acid of the hydrolase with an amino acid, the replacing amino acid binding ~~not strongly retarding~~ cellobiose less tightly than the glycosyl-stabilizing amino acid ~~from leaving the active site~~ to provide a mutant glycosyl hydrolase.

4. (Currently Amended) The method of claim 3, wherein the glycosyl-stabilizing amino acid comprises tyrosine ~~3~~ and the replacing amino acid comprises glycine.

5. (Currently Amended) The methods of claims ~~1 and~~ 3, wherein the replacing step comprises replacing by site-directed-mutagenesis.

6. (Currently Amended) The methods of claims ~~1 and~~ 3, wherein the mutant glycosyl hydrolase comprises a mutant EI endoglucanase.

7. (Currently Amended) The methods of claims ~~1 and~~ 3, wherein the mutant glycosyl hydrolase comprises SEQ ID NO: 2-Y245G, SEQ ID NO: 3 Y42R, SEQ ID NO: 4 W82R, or a mixture thereof.

8. (Currently Amended) The methods of claims ~~1 and~~ 3, wherein the substrate comprises pretreated biomass.

9. (Withdrawn) A mutant glycosyl hydrolase having enhanced catalytic activity, said mutant glycosyl hydrolase comprising an amino having a positively charged amino acid at a position occupied by a hydrophobic surface binding amino acid in a wild-type

glycosyl hydrolase amino acid sequence, wherein said mutant glycosyl hydrolase has an enhanced catalytic activity of 10% to 50% compared to catalytic activity of the wild-type glycosyl hydrolase.

10. (Withdrawn) The mutant glycosyl hydrolase of claim 9 further defined as a cellulase.

11. (Withdrawn) The mutant glycosyl hydrolase of claim 9 further defined as Y245G.

12. (Withdrawn) The mutant ~~glycosly~~ glycosyl hydrolase of claim 9 further defined as Y42R.

13. (Withdrawn) The mutant glycosyl hydrolase of claim 9 further defined as a mannanase.

14. (Withdrawn) The mutant glycosyl hydrolase of claim 9 further defined as comprising W82R.

15 (Withdrawn) A method for converting a biomass into ethanol comprising: a. mixing a composition comprising biomass with a mutant glycosyl hydrolase having enhanced catalytic activity over a wild-type glycosyl hydrolase to provide a soluble fermentable sugar preparation; and b. fermenting said soluble fermentable sugar preparation to provide a composition comprising ethanol.

16. (Withdrawn) The method of claim 15 wherein the biomass is a cellulosic biomass.

17. (Withdrawn) The method of claim 15 wherein the mutant glycosyl hydrolase is Y245G.

18. (Withdrawn) The method of claim 15 wherein the mutant glycosyl hydrolase is Y82R.

19. (Withdrawn) The method of claim 15 wherein the mutant glycosyl hydrolase is W42R.

20. (Withdrawn) The method of claim 15 wherein the mutant glycosyl hydrolase comprises Y245G, Y82R, or W42R.

21. (Withdrawn) The method of claim 15 wherein the biomass is further admixed with a glycohydrolase.

22-25. (Cancelled)

26. (Withdrawn) A method for increasing the specific activity of a hydrolytic depolymerizing enzyme, comprising replacing an extended-active site residue that binds strongly to the leaving group with another that binds much less strongly to the leaving group.

27. (Withdrawn) A method for increasing the specific activity of a glycosyl hydrolase on a pretreated biomass substrate, comprising:

replacing, via site directed mutagenesis, a hydrophobic surface binding amino acid of the hydrolase with a positively charged amino acid arginine, the hydrophobic surface binding amino acid of the hydrolase selected from the group consisting of tryptophan and tyrosine, the hydrolase selected from the group consisting of an EI endoglucanase, Y245G, Y42R, W82R, and a mixture thereof; and

replacing, via site directed mutagenesis, an active site associated glycosyl-stabilizing amino acid of the hydrolase including tyrosine with an amino acid including glycine, the glycine not strongly retarding cellobiose from leaving the active site,

to produce a mutant glycosyl hydrolase having enhanced catalytic activity, the mutant glycosyl hydrolase comprising an amino having a positively charged amino acid at a position occupied by a hydrophobic surface binding amino acid in a wild-type glycosyl hydrolase amino acid sequence, wherein said mutant glycosyl hydrolase has an enhanced catalytic activity of 10% to 50% compared to catalytic activity of the wild-type glycosyl hydrolase.

28. (Withdrawn) The method of claim 27, further comprising steps of

mixing a composition comprising biomass with the mutant glycosyl hydrolase having enhanced catalytic activity over a wild-type glycosyl hydrolase to provide a soluble fermentable sugar preparation; and

fermenting the soluble fermentable sugar preparation to provide a composition comprising ethanol.

29. (New) A method for increasing the specific activity of an EI endoglucanase or a structural analog thereof on a biomass, comprising replacing, by site-directed-mutagenesis, an active site associated glycosyl-stabilizing amino acid of the endoglucanase with an amino acid, the replacing amino acid binding cellobiose less tightly than the glycosyl-stabilizing amino acid to provide a mutant endoglucanase.

30. (New) The method of claim 29, wherein the glycosyl-stabilizing amino acid comprises tyrosine and the replacing amino acid comprises glycine.

31. (New) The method of claim 29, wherein the mutant endoglucanase comprises SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, or a mixture thereof.

Amendments to the Specification:

On pages 28-30 of the Specification, please replace the paragraphs including all of Example 7 in its entirety beginning at "Example 7" and ending prior to "BIBLIOGRAPHY" with the fiollowing paragraphs. These paragraphs include paragraphs 72-80 in the published application. There are no deletions in the text below, and additons are indicated by double underlining because portions of the inserted text contain native underlining.

EXAMPLE 7

Sequence Information

The following table provides sequence data referenced throughout the present specification.

Nucleic acid sequence for EI endoglucanase

5'-

GCGGGCGGCGGCTATTGGCACACGAGCGGCCGGGAGATCCTGGACGCGAAC
AACGTGCCGGTACGGATCGCCGGCATCAACTGGTTTGGGTTCGAAACCTGCA
ATTACGTCGTGCACGGTCTCTGGTCACGCGACTACCGCAGCATGCTCGACCA
GATAAAGTCGCTCGGCTACAACA- CAATCCGGCTGCCGTACTCTGACGAC
ATTCTCAAGCCGGGCACCATGCCGAACAGCATCAATTTTTACCAGATGAATC
AGGACCTGCAGGGTCTGACGTCCTTGCAGGTCATGGACAAAATCGTCGCGTA
CGCCGGTCAGATCGGCCTGCGCATCATTCTTGACCGCCACCGACCGGATTGC
AGCGGGCAGTCGGCGCTGTGGTACACGAGCAGCGTCTCGGAG- GCTACGT
GGATTTCCGACCTGCAAGCGCTGGCGCAGCGCTACAAGGGAAACCCGACG-
GTCGTCGGCTTTGACTTGCACAACGAGCCGCATGACCCGGCCTGCTGGGGCT
GCGGCGATCCGAGCATCGACTGGCGATTGGCCGCCGAGCGGGCCGGAAACG
CCGTGCTCTCG- GTGAATCCGAACCTGCTCATTTTCGTCGAAGGTGTGCAGA
GCTACAACGGAGACTCCTACTGGTGGGGCGGCAACCTGCAAGGAGCCGGCC
AGTACCCGGTCGTGCTGAACGTGCCGAACCGCCTGGTGTACTCGGCGCACGA
CTACGCGACGAGCGTCTACCCGCAGACGTGGTTCAGCGATCCGACCTTCCCC
AACAACATGCCCGGCATCTGGAACAAGAACTGGGGATACCTCTTCAATC

AGAACATTGCACCGGTATGGCTGGGCGAATTCGGTACGACACTGCAATCCAC
GACCGACCAGACGTTGGCTGAAGACGCTCGTCCAGTACCTACGGCCGACCGC
GCAATACGGTGCGGACAGCTTCCAGTGGACCTTCTGGTCCTGGAACCCCGAT
TCCGGCGACACAGGAGGAATTCTCAAGGATGACTGGCAGACGGTCGACACA
GTAAAAGACGGCTATCTCGCGCCGATCAAGTCGTCGATTTTCGATCCTGTCTA
ATGAATCGCCTAGCAGTCAACCGTCCCCGTCGGTGTCGCCGTCTCCGTCGCCG
AGCCCGTCGGCGAGTCGGACGCCGACGCCTACTCCGACGCCGACAGCCAGCC
CGACGCCAACGCTGACCCCTACTGCTACGCCCACGCCCACGGCAAGCCCGAC
GCCGTCACCGACGGCAGCCTCCGGAGCCCGCTGCACCGCGAGTTACCAGGTC
AACAGCGATTGGGGCAATGGCTTCACGGTAACGGTGGCCGTGACAAATTCCG
-3' [SEQ ID NO. 1]

Amino acid sequence for EI endoglucanse

5'-
AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNYVVHGLWSRDYRSMLDQI
KSLGYNTIRLPYSDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIG
LRIILDRHRPDCSGQSALWYTSSVSEATWISDLQALAQRYKGNPTVVGFDLHNEP
HDPACWGCGDPSIDWRLAAERAGNAVLSVNPNLLIFVEGVQSYNGDSY
WWGGNLQGAGQYPVVLNVPNRLVYSAHDYATSVYPQTWFSDPTFPNNMPGIW
NKNWGYLFNQNIAPVWLGEFGTTLQSTTDQTWLKTLVQYLRPTAQYGADSFQW
TFWSWNPDSGDTGGILKDDWQTVDTVKDGYLA PIKSSIFDPVG-3' [SEQ ID NO.
2-

DNA sequence for Y245G Mutant with mutation site underlined.

5.-
GCGGGCGGCGGCTATTGGCACACGAGCGGCCGGGAGATCCTGGACGCGAAC
AACGTGCCGGTACGGATCGCCGGCATCAACTGGTTTGGGTTCGAAACCTGCA
ATTACGTCGTGCACGGTCTCTGGTCACGCGACTACCGCAGCATGCTCGACCA
GATAAAGTCGCTCGGCTACAACA- CAATCCGGCTGCCGTACTCTGACGAC
ATTCTCAAGCCGGGCACCATGCCGAACAGCATCAATTTTTACCAGATGAATC
AGGACCTGCAGGGTCTGACGTCCTTGCAGGTCATGGACAAAATCGTCGCGTA

CGCCGGTCAGATCGGCCTGCGCATCATTCTTGACCGCCACCGACCGGATTGC
AGCGGGCAGTCGGCGCTGTGGTACACGAGCAGCGTCTCGGAGGCTACGT
GGATTTCCGACCTGCAAGCGCTGGCGCAGCGCTACAAGGGAAACCCGACG-
GTCGTCGGCTTTGACTTGCACAACGAGCCGCATGACCCGGCCTGCTGGGGCT
GCGGCGATCCGAGCATCGACTGGCGATTGGCCGCCGAGCGGGCCGGAAACG
CCGTGCTCTCG- GTGAATCCGAACCTGCTCATTTTCGTCGAAGGTGTGCAGA
GCTACAACGGAGACTCCTACTGGTGGGGCGGCAACCTGCAAGGAGCCGGCC
AGTACCCGGTCGTGCTGAACGTGCCGAACCGCCTGGTGTACTCGGCGCACGA
CTACGCGACGAGCGTCGGCCCGCAGACGTGGTTCAGCGATCCGACCTTCCCC
AACAACATGCCCGGCATCTGGAACAAGAACTGGGGATACCTCTTCAATCAGA
ACATTGCACCGGTATGGCTGGGCGAATTCGGTACGACACTGCAATCCACGAC
CGACCAGACGTGGCTGAAGACGCTCGTCCAGTACCTACGGCCGACCGCGCAA
TACGGTGCGGACAGCTTCCAGTGGACCTTCTGGTCCTGGAACCCCGATTCCG
GCGACACAGGAGGAATTCTCAAGGATGACTGGCAGACGGTCGACACAGTAA
AAGACGGCTATCTCGCGCCGATCAAGTCGTCGATTTTCGATCCTGTCTAATGA
ATCGCCTAGCAGTCAACCGTCCCCGTCGGTGTCGCCGTCTCCGTCGCCGAGCC
CGTCGGCGAGTCGGACGCCGACGCCTACTCCGACGCCGACAGCCAGCCCGAC
GCCAACGCTGACCCCTACTGCTACGCCCACGCCCACGGCAA
GCCCGACGCCGTCACCGACGGCAGCCTC-
CGGAGCCCGCTGCACCGCGAGTTACCAGGTCAACAGCGATTGGGGCAAT-3'
[SEQ ID NO. 2]

Translated amino acid sequence for Y245G mutation, with modification underlined.

5'-
AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNYVVHGLWSRDYRSMLDQI
KSLGYNTIRLPYSDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIG
LRIILDRHRPDCSGQSALWYTSSVSEATWISDLQALAQRYKGNPTVVGFDLHNEP
HDPACWGCGDPSIDWRLAAERAGNAVLSVNPNLLIFVEGVQSYNGDSYWWGG
NLQGAGQYPVVLNVPNRLVYSAHDYATSVGPQTWFSDPTFPNNMPGIWNKNW

GYLFNQNIAPVWLGEFGTTLQSTTDQTWLKTLVQYLRPTAQYGADSFQWTFWS
WNPDSGDTGGILKDDWQTVDTVKDGYLA PIKSSIFDPV-3' [SEQ ID NO. 2]

DNA sequence for W42R Mutant with mutation site underlined

5'-

GCGGGCGGCGGCTATTGGCACACGAGCGGCCGGGAGATCCTGGACGCGAAC
AACGTGCCGGTACGGATCGCCGGCATCAACTGGTTTGGGTTCGAAACCTGCA
ATTACGTCGTGCACGGTCTCCGGTCACGCGACTACCGCAGCATGCTCGACCA
GATAAAGTCGCTCGGCTACAACACAATCCGGCTGCCGTACTCTGACGAC
ATTCTCAAGCCGGGCACCATGCCGAACAGCATCAATTTTTACCAGATGAATC
AGGACCTGCAGGGTCTGACGTCCTTGCAGGTCATGGACAAAATCGTCGCGTA
CGCCGGTCAGATCGGCCTGCGCATCATTCTTGACCGCCACCGACCGGATTGC
AGCGGGCAGTCGGCGCTGTGGTACACGAGCAGCGTCTCGGAGGCTACGTGGA
TTTCCGACCTGCAAGCGCTGGCGCAGCGCTACAAGGGAAACCCGACGGTCGT
CGGCTTTGACTTGCACAACGAGCCGCATGACCCGGCCTGCTGGGGCTGCGGC
GATCCGAGCATCGACTGGCGATTGGCCGCCGAGCGGGCCGGAAACGCCGTGC
TCTCGGTGAATCCGAACCTGCTCATTTTCGTCGAAGGTGTGCAGAGCTACAAC
GGAGACTCCTACTGGTGGGGCGGCAACCTGCAAGGAGCCGGCCAGTACCCG
GTCGTGCTGAACGTGCCGAACCGCCTGGTGTACTCGGCGCACGACTACGCGA
CGAGCGTCTACCCGCAGACGTGGTTCAGCGATCCGACCTTCCCCAACAACAT
GCCCGGCATCTGGAACAAGAACTGGGGATACCTCTTCAATCAGAACATTGCA
CCGGTATGGCTGGGCGAATTCGGTACGACACTGCAATCCACGACCGACCAGA
CGTGGCTGAAGACGCTCGTCCAGTACCTACGGCCGACCGCGCAATACGGTGC
GGACAGCTTCCAGTGGACCTTCTGGTCCTGGAACCCCGATTCCGGCGACACA
GGAGGAATTCTCAAGGATGACTGGCAGACGGTCGACACAGTAAAAGACGGC
TATCTCGCGCCGATCAAGTCGTCGATTTTCGATCCTGTCTAATGAATCGCCTA
GCAGTCAACCGTCCCCGTCGGTGTCGCCGTCTCCGTCGCCGAGCCCGTCGGC
GAGTCGGACGCCGACGCCTACTCCGACGCCGACAGCCAGCCCGACGCCAACG
CTGACCCCTACTGCTACGCCCACGCCCACGGCAAGCCCGACGCCGTCACCGA
CGGCAGCCTCCGGAGCCCGCTGCACCGCGAGTTACCAGGTCAACAGCGATTG

GGGCAATGGCTTCACGGTAACGGTGGCCGTGACAAATTCCG-3' [SEQ ID NO. 31]

Translated amino acid sequence for W42R mutation, with modification underlined.

5'-

AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNYVVHGLRSRDYRSMLDQIK
SLGYNTIRLPYSDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIGL
RIILDRHRPDCSGQSALWYTSSVSEATWISDLQALAQRYKGNPTVVGFDLHNEPH
DPACWGCGDPSIDWRLAAERAGNAVLSVNPNLLIFVEGVQSYNGDSYWWGGN
LQGAGQYPVVLNVPNRLVYSAHDYATSVYPQTWFSDPTFPNNMPGIWNKNWG
YLFNQNIAPVWLGEFGTTLQSTTDQTWLKTLVQYLRPTAQYGADSFQWTFWSW
NPDSGDTGGILKDDWQTVDTVKDGYLAPIKSSIFDPV-3' [SEQ ID NO. 31]

DNA sequence for Y82R Mutant with mutation site underlined.

5'-

GCGGGCGGCGGCTATTGGCACACGAGCGGCCGGGAGATCCTGGACGCGAAC
AACGTGCCGGTACGGATCGCCGGCATCAACTGGTTTGGGTTCGAAACCTGCA
ATTACGTCGTGCACGGTCTCTGGTCACGCGACTACCGCAGCATGCTCGACCA
GATAAAGTCGCTCGGCTACAACACAATCCGGCTGCCGTACTCTGACGACATT
CTCAAGCCGGGCACCATGCCGAACAGCATCAATTTTCGGCAGATGAATCAGG
ACCTGCAGGGTCTGACGTCCTTGCAGGTCATGGACAAAATCGTCGCGTACGC
CGGTCAGATCGGCCTGCGCATCATTCTTGACCGCCACCGACCGGATTGCAGC
GGGCAGTCGGCGCTGTGGTACACGAGCAGCGTCTCGGAGGCTACGTGGATTT
CCGACCTGCAAGCGCTGGCGCAGCGCTACAAGGGAAACCCGACGGTCGTCG
GCTTTGACTTGCACAACGAGCCGCATGACCCGGCCTGCTGGGGCTGCGGCGA
TCCGAGCATCGACTGGCGATTGGCCGCCGAGCGGGCCGGAAACGCCGTGCTC
TCGGTGAATCCGAACCTGCTCATTTTCGTCGAAGGTGTGCAGAGCTACAACG
GAGACTCCTACTGGTGGGGCGGCAACCTGCAAGGAGCCGGCCAGTACCCGGT
CGTGCTGAACGTGCCGAACCGCCTGGTGTACTCGGCGCACGACTACGCGACG
AGCGTCTACCCGCAGACGTGGTTCAGCGATCCGACCTTCCCCAACAACATGC
CCGGCATCTGGAACAAGAACTGGGGATACCTCTTCAATCAGAACATTGCACC

GGTATGGCTGGGCGAATTCGGTACGACACTGCAATCCACGACCGACCAGACG
TGGCTGAAGACGCTCGTCCAGTACCTACGGCCGACCGCGCAATACGGTGCGG
ACAGCTTCCAGTGGACCTTCTGGTCCTGGAACCCCGATTCCGGCGACACAGG
AGGAATTCTCAAGGATGACTGGCAGACGGTCGACACAGTAAAAGACGGCTAT
CTCGCGCCGATCAAGTCGTCGATTTTCGATCCTGTCTAATGAATCGCCTAGCA
GTCAACCGTCCCCGTCGGTGTCGCCGTCTCCGTCGCCGAGCCCGTCGGCGAGT
CGGACGCCGACGCCTACTCCGACGCCGACAGCCAGCCCGACGCCAACGCTGA
CCCCTACTGCTACGCCCACGCCCACGGCAAGCCCGACGCCGTCACCGACGGC
AGCCTCCGGAGCCCGCTGCACCGCGAGTTACCAGGTCAACAGCGATTGGGGC
AATGGCTTCACGGTAACGGTGGCCGTGACAAATTCCG-3' [SEQ ID NO. 4]

Translated amino acid sequence for Y82R mutation, with modification underlined.

5'-

AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNYVVHGLWSRDYRSMLDQI
KSLGYNTIRLPYSDDILKPGTMPNSINFRQMNQDLQGLTSLQVMDKIVAYAGQIG
LRIILDRHRPDCSGQSALWYTSSVSEATWISDLQALAQRYKGNPTVVGFDLHNEP
HDPACWGCGDPSIDWRLAAERAGNAVLSVNPNLLIFVEGVQSYNGDSYW
WGGNLQGAGQYPVVLNVPNRLVYSAHDYATSVYPQTWFSDPTFPNNMPGIWN
KNWGYLFNQNIAPVWLGEFGTTLQSTTDQTWLKTLVQYLRPTAQYGADSFQWT
FWSWNPDSGDTGGILKDDWQTVDTVKDGYLAPIKSSIFDPV-3' [SEQID NO. 4]